

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file us-10-006-130a-129.res made by tport on Fri 20 Feb 104 15:36:33 -PST.

Query sequence being compared:US-10-006-130A-129 (1-2213)

1. US-10-006-130A-129 (1-2213)		US-09-374-046A-3 Sequence 3, Application US/09374046A	
Initial Score	= 1731	Optimized Score	= 2150 Significance = 18.90
Residue Identity	= 95% Matches	= 2204 Mismatches	= 9
Gaps	= 106 Conservative Substitutions	= 0	= 0
X	10 20 30 40 50 60 70		
GAGCGACATGGCAAGCCGTTGGCGGTTTGCGTGTCTGTGACCATGGTGTGGGTGCTCATCGTTT			
GAGCGACATGGCAAGCGTTGGCGTTTGCGTGTCTGTGACCATGGTGTGGGTGCTCATCGTTT			
X	10 20 30 40 50 60 70		
GCGACGTTCCCTAGCCTCTGCCAAGAAAGAAGGAGATGGTGTATCTGAAAAGGTAGTCAGTRGATGG			
GCGACGTTCCCTAGCCTCTGCCAAGAAAGAAGGAGATGGTGTATCTGAAAAGGTAGTCAGTRGATGG			
X	80 90 100 110 120 130 140		
AATGGACTAACAAAGAACCTGTAAATAGAATGAAATGAAATGAACTCGAGAACAGTTCGCGCTGTGAAAGGCCAACCGA			
AATGGACTAACAAAGAACCTGTAAATAGAATGAAATGAAATGAACTCGAGAACAGTTCGCGCTGTGAAAGGCCAACCGA			
X	90 100 110 120 130 140		
AATGGACTAACAAAGAACCTGTAAATAGAATGAAATGAAATGAACTCGAGAACAGTTCGCGCTGTGAAAGGCCAACCGA			
AATGGACTAACAAAGAACCTGTAAATAGAATGAAATGAAATGAACTCGAGAACAGTTCGCGCTGTGAAAGGCCAACCGA			
X	150 160 170 180 190 200 210		
ATGAAATTCTGGTATCGTCATGTTACTGCCTCCAACTCAGTGCATTAGACAGTCAGTGCCTGTGAAAGGCCAACCGA			
ATGAAATTCTGGTATCGTCATGTTACTGCCTCCAACTCAGTGCATTAGACAGTCAGTGCCTGTGAAAGGCCAACCGA			
X	220 230 240 250 260 270 280		
ATGAAAGATTCCAGATCCTGGCAAACCTGGCATACTCAGTGCATTAGACAGTCAGTGCCTGTGAAAGGCCAACCGA			
ATGAAAGATTCCAGATCCTGGCAAACCTGGCATACTCAGTGCATTAGACAGTCAGTGCCTGTGAAAGGCCAACCGA			
X	220 230 240 250 260 270 280		
ATGAAAGATTCCAGATCCTGGCAAACCTGGCATACTCAGTGCATTAGACAGTCAGTGCCTGTGAAAGGCCAACCGA			
ATGAAAGATTCCAGATCCTGGCAAACCTGGCATACTCAGTGCATTAGACAGTCAGTGCCTGTGAAAGGCCAACCGA			
X	290 300 310 320 330 340 350 360		
TGGTGGATTGGTGTGAAGGCTCTGTGTATTCTAGATGCTAAACATGTTACGTCAGCTCCAACTTCATCAACT			
TGGTGGATTGGTGTGAAGGCTCTGTGTATTCTAGATGCTAAACATGTTACGTCAGCTCCAACTTCATCAACT			
X	290 300 310 320 330 340 350 360		
TGGTGGATTGGTGTGAAGGCTCTGTGTATTCTAGATGCTAAACATGTTACGTCAGCTCCAACTTCATCAACT			
TGGTGGATTGGTGTGAAGGCTCTGTGTATTCTAGATGCTAAACATGTTACGTCAGCTCCAACTTCATCAACT			
X	370 380 390 400 410 420 430		
TTTCTGGCAAAGGGAAACCCAAACGCCGTTGATACATGAGTTACAGGGTGGGGTTTTCAGCTGAGCGAGA			
TTTCTGGCAAAGGGAAACCCAAACGCCGTTGATACATGAGTTACAGGGTGGGGTTTTCAGCTGAGCGAGA			
X	440 450 460 470 480 490 500		
TTTCTGGCAAACGCCGTTGATCGCGACAGAACCTGGCTGAGCGAGA			
TTTCTGGCAAACGCCGTTGATCGCGACAGAACCTGGCTGAGCGAGA			
X	510 520 530 540 550 560 570		

	SEARCH STATISTICS									
	Mean	Median	Standard Deviation	CPU	Total Elapsed					
Scores:	48	42	89.04							
Times:										
Similarity matrix	Unitary	K-tuple	4							
Mismatch penalty	1	Joining penalty	30							
Gap penalty	5.00	Window size	500							
Gap size penalty	0.33									
Cutoff score	1									
Randomization group	0									
PARAMETERS										
SCORE	0 192 385 577 769 962 1154 1346 1539 1731									
STDEV	0 1 2 3 4 5 6 7 8 9									

510 520 530 540 550 560 570
 580 590 600 610 620 630 640 1440 1450 1460 1470 1480 1490 1500 1510
 TTATGTTGGGTTGGCTTGGCTTGGTATTCTGGACTTGTTATCTGGATGTTATCTGGAAAGTAATATGGAAATTCTCT
 TTATGTTGGGTTGGCTTGGCTTGGTATTCTGGACTTGTTATCTGGAAAGTAATATGGAAATTCTCT
 580 590 600 610 620 630 640 1450 1460 1470 1480 1490 1490 1500 1510
 650 660 670 680 690 700 710 720
 TTATAAAACCGATGGGCTTGGCTTGGCTTGGTATTCTGGACTTGTTATCTGGAAAGTAATATGGAAATTCTCT
 TTATAAAACCGATGGGCTTGGCTTGGCTTGGTATTCTGGACTTGTTATCTGGAAAGTAATATGGAAATTCTCT
 650 660 670 680 690 700 710 720
 730 740 750 760 770 780 790 1520 1530 1540 1550 1560 1570 1580
 ATATAAGGAAACCATTGCCATAGAATCCCCAACCGGACATGTGAATTATCCATGGAAAGCCTC
 ATATAAGGAAACCATTGCCATAGAATCCCCAACCGGACATGTGAATTATCCATGGAAAGCCTC
 730 740 750 760 770 780 790 1530 1540 1550 1560 1570 1580
 800 810 820 830 840 850 860
 AGGCCAGTTGTTAGCTGAACACACATTTGTTCTCTGTTTAATGGGAGCTTACCTTAGGAATGGTGCCTT
 AGGCCAGTTGTTAGCTGAACACACATTTGTTCTCTGTTTAATGGGAGCTTACCTTAGGAATGGTGCCTT
 800 810 820 830 840 850 860 1590 1600 1610 1620 1630 1640 1650
 870 880 890 900 910 920 930
 TATGTGAAGCTCTTACCTCTACATGGATTAGCTGAAGGATAATGTTGGCTGCTGTTGGACTCTG
 TATGTGAAGCTCTACCTCTACATGGATTAGCTGAAGGATAATGTTGGCTGCTGTTGGACTCTG
 870 880 890 900 910 920 930 1640 1650 1660 1670 1680 1690 1700 1720
 940 950 960 970 980 990 1000
 TTGTATTATTCTTCAGTGGATGCTCTATTAGCTTAATATCATGGTACCCATACGGTTCTG
 TTGTATTATTCTTCAGTGGATGCTCTATTAGCTTAATATCATGGTACCCATACGGTTCTG
 940 950 960 970 980 990 1000 1700 1710 1720 1730 1740 1750 1760
 1010 1020 1030 1040 1050 1060 1070 1080
 TGAGTTAAAGGTCCCAGACATATAGACACTGGGATGACTGGAAATTGAAAGGAATATCTGGTGTGT
 TGAGTTAAAGGTCCCAGACATATAGACACTGGGATGACTGGAAATTGAAAGGAATATCTGGTGTGT
 1010 1020 1030 1040 1050 1060 1070 1080 1770 1780 1790 1800 1810 1820 1830 1840
 1090 1100 1110 1120 1130 1140 1150
 TGAAAAGAAGATGCAACTGTGTTATTTGTATTACCTC-TTTTTTCACTGTTAAATAGTTAAATCAT
 TGAAAAGAAGATGCAACTGTGTTATTTGTATTACCTC-TTTTTTCACTGTTAAATAGTTAAATCAT
 1090 1100 1110 1120 1130 1140 1150 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940
 1160 1170 1180 1190 1200 1210 1220
 TTAAACCAAAGAGATGTGAGTGGCTTAAACAGCAATCCCTGTCATAAAATCTGGATGTTGGAAATAATA
 TTAAACCAAAGAGATGTGAGTGGCTTAAACAGCAATCCCTGTCATAAAATCTGGATGTTGGAAATAATA
 1160 1170 1180 1190 1200 1210 1220 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980
 1230 1240 1250 1260 1270 1280 1290
 TCCTCTTAACCTCTCTCCAGTGAACCTTATGGAAACATTAAATTAGTACCATTAAGTATATAAA
 TTAAACCAAAGAGATGTGAGTGGCTTAAACAGCAATCCCTGTCATAAAATCTGGATGTTGGAAATAATA
 TTAAACCAAAGAGATGTGAGTGGCTTAAACAGCAATCCCTGTCATAAAATCTGGATGTTGGAAATAATA
 1230 1240 1250 1260 1270 1280 1290 1990 2000 2010 2020 2030 2040 2050
 1300 1310 1320 1330 1340 1350 1360
 TTGTAAACACTACTACTTTGTTAGTTAGTGAACAAAGCTCAAAACTACTTTAGTTAACTTGGTCATCTGATT
 TTGTAAACACTACTACTTTGTTAGTTAGTGAACAAAGCTCAAAACTACTTTAGTTAACTTGGTCATCTGATT
 1300 1310 1320 1330 1340 1350 1360 2060 2070 2080 2090 2100 2110 2120
 1370 1380 1390 1400 1410 1420 1430
 TATATTGCCTTATCCAAAGATGGGAAAGTAAGTCCTGACCAAGGTGTTCCACATATGCCGTGTAAGATAA
 TATATTGCCTTATCCAAAGATGGGAAAGTAAGTCCTGACCAAGGTGTTCCACATATGCCGTGTAAGATAA
 1370 1380 1390 1400 1410 1420 1430 1440

